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In the Specification:

Change 1: Please insert the following seven paragraphs into the specification at page 3, line 26 as follows:

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E show consecutive segments of sequence alignment for two BASB029 polynucleotides, SEQ ID NO:1 and 3.

Figures 2A-2B show consecutive segments of sequence alignment for two BASB029 polypeptides, SEQ ID NO:2 and 4.

Figure 3 shows expression and purification of recombinant BASB029 in E. coli. A substantially purified BASB029 protein fraction (more than 80%) was separated on a 4-20% gradient polyacrylamide gel (NOVEX) under PAGE-SDS conditions in parallel to a protein molecular weight marker. Gels were either stained with Coomassie Blue R250 (lane 1) or analyzed by western blot using an anti-(His5) monoclonal antibody (lane 2).

Figure 4 shows recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera.

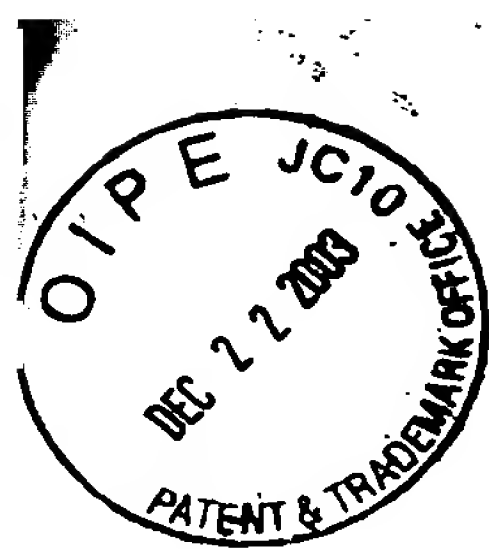
Figure 5 shows recognition of the BASB029 protein on several NmB strains with BASB029 immunized mice sera.

Figure 6 shows anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

Figure 7 shows anti-BASB029 antibodies in convalescent sera (part B) and in immunized mice (part A).

Change 2: Please insert the following paragraph at page 57, line 2:

What is claimed is:



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Figure 1A

Identity to SeqID No:1 is indicated by a dot, and a dash ("-") indicates a missing nucleotide.

```

          *          20          *          40          *
Seqid1 : ATGAACAAAATATACCGCATCATTTGGAATAGTGCCCTCAATGCCTGGGT : 50
Seqid3 : ..... : 50

          60          *          80          *          100
Seqid1 : CGCCGTATCCGAGCTCACACGCAACCACACCAAACGCGCCTCCGCAACCG : 100
Seqid3 : ..... : 100

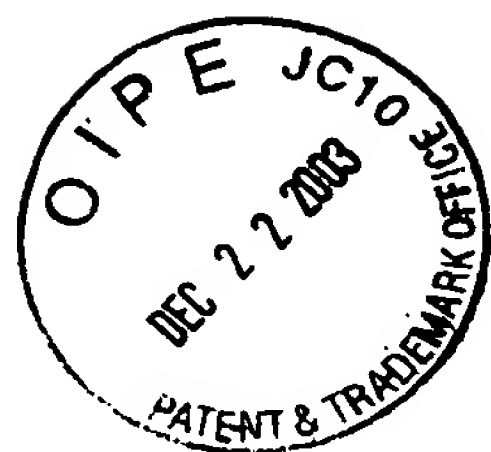
          *          120          *          140          *
Seqid1 : TGGCGACCGCCGTATTGGCGACACTGTTGTTTGCAACGGTTCAGGCGAGT : 150
Seqid3 : ..AA.....A... : 150

          160          *          180          *          200
Seqid1 : ACTACCGAT-----GACGACGATTTATATTTAGAACCCGTACAACG : 191
Seqid3 : G...A.A..GAAGAGCAA..A..A.....C..... : 200

          *          220          *          240          *
Seqid1 : CACTGCTGTCGTGTTGAGCTTCCGTTCCGATAAAGAAGGCACGGGAGAAA : 241
Seqid3 : .....T..C.....TAG..AA..... : 250

          260          *          280          *          300
Seqid1 : AAG---AAGTTACAGAAGATTCAAATTGGGGAGTATATTTGACAAGAAA : 288
Seqid3 : ...AAA....AGA....A.....G.....C.....A..G..... : 300

          *          320          *          340          *
Seqid1 : GGAGTACTAACAGCCGGAACAATCACCTCAAAGCCGGCGACAACCTGAA : 338
Seqid3 : .....A..GA..... : 350
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Figur 1B

360 * 380 * 400
Seqid1 : AATCAAACAAAACACCAATGAAAACACCAATGCCAGTAGCTTCACCTACT : 388
Seqid3 :-----G..CA.A..... : 382

* 420 * 440 *
Seqid1 : CGCTGAAAAAAGACCTCACAGATCTGACCAGTGTTGGAAGTGAATAA : 438
Seqid3 : : 432

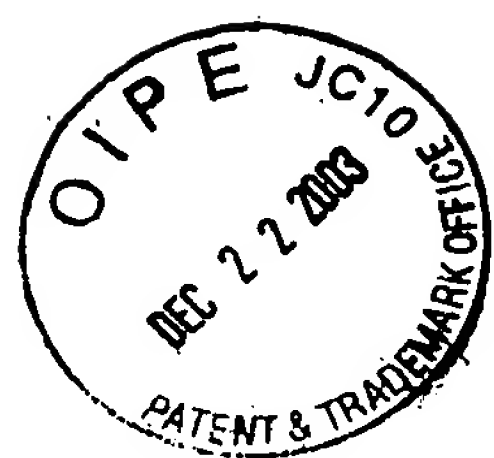
460 * 480 * 500
Seqid1 : TCGTTTAGCGCAAACAGCAATAAAGTCAACATCACAAGCGACACCAAAGG : 488
Seqid3 :G..... : 482

* 520 * 540 *
Seqid1 : CTTGAATTTTCGCGAAAAAACGGCTGAGACCAACGGCGACACCACGGTTC : 538
Seqid3 :T.....G.....G...G..... : 532

560 * 580 * 600
Seqid1 : ATCTGAACGGTATCGGTTGACTTTGACCGATACGCTGCTGAATACCGGA : 588
Seqid3 : .C.....T..... : 582

* 620 * 640 *
Seqid1 : GCGACCACAAACGTAACCAACGACAACGTTACCGATGACGAGAAAAAACG : 638
Seqid3 : : 632

660 * 680 * 700
Seqid1 : TGCGGCAAGCGTTAAAGACGTATTAAACGCAGGCTGGAACATTAAAGGCG : 688
Seqid3 : : 682

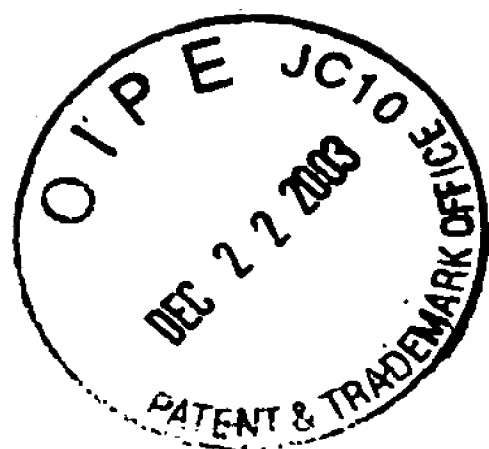


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Figure 1C

	*	720	*	740	*
Seqid1	:	TTAAACCCGGTACAACAGCTTCCGATAACGTTGATTTTCGTCCGCACTTAC	:	738	
Seqid3	:	:	732	
		760	*	780	*
Seqid1	:	GACACAGTCGAGTTCTTGAGCGCAGATACGAAAACAACGACTGTTAATGT	:	788	
Seqid3	:	:	782	
			*	820	*
Seqid1	:	GGAAAGCAAAGACAACGGCAAGAGAACCGAAGTTAAATCGGTGCGAAGA	:	838	
Seqid3	:A.....	:	832	
			*	860	*
Seqid1	:	CTTCTGTTATCAAAGAAAAAGACGGTAAGTTGGTTACTGGTAAAGACAAA	:	888	
Seqid3	:T.....	:	882	
			*	920	*
Seqid1	:	GGCGAGAATGATTCTTCTACAGACAAAGGCGAAGGCTTAGTGACTGCAAA	:	938	
Seqid3	:G.....G.....	:	932	
			*	960	*
Seqid1	:	AGAAGTGATTGATGCAGTAAACAAGGCTGGTTGGAGAATGAAAACAACAA	:	988	
Seqid3	:	:	982	
			*	1020	*
Seqid1	:	CCGCTAATGGTCAAACAGGTCAAGCTGACAAGTTTGAAACCGTTACATCA	:	1038	
Seqid3	:	:	1032	
			*	1060	*
Seqid1	:	GGCACAAATGTAACCTTTGCTAGTGGTAAAGGTACAACCTGCGACTGTAAG	:	1088	
Seqid3	:	:	1082	



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Figure 1D

 * 1120 * 1140 *
Seqid1 : TAAAGATGATCAAGGCAACATCACTGTTATGTATGATGTAAATGTCGGCG : 1138
Seqid3 : : 1132

 1160 * 1180 * 1200
Seqid1 : ATGCCCTAAACGTCAATCAGCTGCAAAACAGCGGTTGGAATTTGGATTCC : 1188
Seqid3 : : 1182

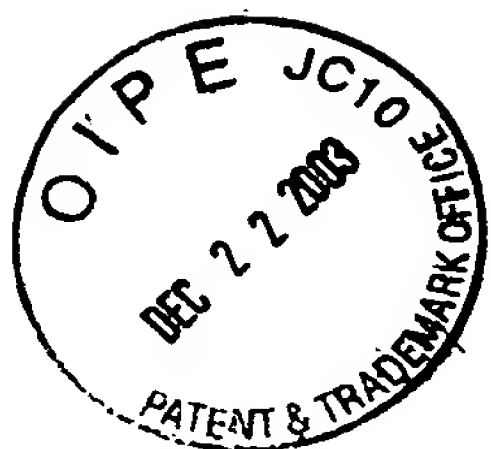
 * 1220 * 1240 *
Seqid1 : AAAGCGGTTGCAGGTTCTTCGGGCAAAGTCATCAGCGGCAATGTTTCGCC : 1238
Seqid3 : : 1232

 1260 * 1280 * 1300
Seqid1 : GAGCAAGGGAAAGATGGATGAAACCGTCAACATTAATGCCGGCAACAACA : 1288
Seqid3 : : 1282

 * 1320 * 1340 *
Seqid1 : TCGAGATTACCCGCAACGGCAAAAATATCGACATCGCCACTTCGATGACC : 1338
Seqid3 :T..... : 1332

 1360 * 1380 * 1400
Seqid1 : CCGCAATTTTCCAGCGTTTCGCTCGGCGCGGGGGCGGATGCGCCCACTTT : 1388
Seqid3 :G..... : 1382

 * 1420 * 1440 *
Seqid1 : AAGCGTGGATGACGAGGGCGCGTTGAATGTCGGCAGCAAGGATGCCAACA : 1438
Seqid3 : G.....---.G..A...A.....A.G.A..... : 1429



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Figure 1E

1460 * 1480 * 1500
Seqid1 : AACCCGTCCGCATTACCAATGTCGCCCCGGGCGTTAAAGAGGGGGATGTT : 1488
Seqid3 : : 1479

* 1520 * 1540 *
Seqid1 : ACAAACGTCGCACAACCTTAAAGGCGTGGCGCAAACTTGAACAACCACAT : 1538
Seqid3 :G... : 1529

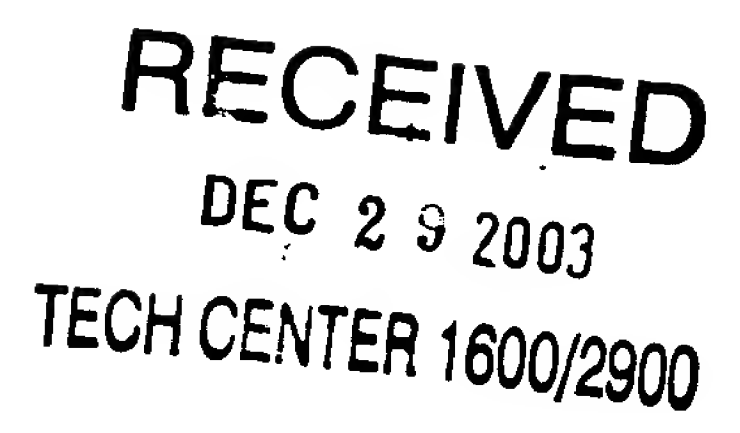
1560 * 1580 * 1600
Seqid1 : CGACAATGTGGACGGCAACGCGCGTGCGGGCATCGCCCAAGCGATTGCAA : 1588
Seqid3 : : 1579

* 1620 * 1640 *
Seqid1 : CCGCAGGTCTGGTTCAGGCGTATCTGCCCGGCAAGAGTATGATGGCGATC : 1638
Seqid3 :T..... : 1629

1660 * 1680 * 1700
Seqid1 : GGCGGCGGCACTTATCGCGGCGAAGCCGGTTATGCCATCGGCTACTCAAG : 1688
Seqid3 :C.....C.. : 1679

* 1720 * 1740 *
Seqid1 : CATTTCCGACGGCGGAAATTGGATTATCAAAGGCACGGCTTCCGGCAATT : 1738
Seqid3 : T..... : 1729

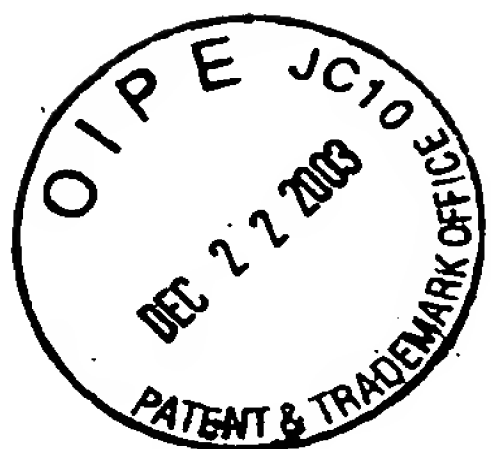
1760 * 1780 *
Seqid1 : CGCGCGGCCATTTTCGGTGCTTCCGCATCTGTCGGTTATCAGTGGTAA : 1785
Seqid3 : : 1776



```

          *           320           *           340           *
Seqid2  :  GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTS  :  346
Seqid4  :  ...G...E..... :  344

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Figure 2B

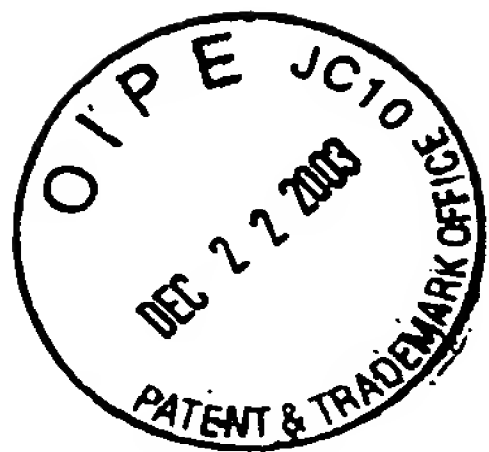
360 * 380 * 400
Seqid2 : GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDS : 396
Seqid4 : : 394

* 420 * 440 *
Seqid2 : KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSM : 446
Seqid4 : : 444

460 * 480 * 500
Seqid2 : PQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKEGDV : 496
Seqid4 :GD-.....KD..... : 493

* 520 * 540 *
Seqid2 : TNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAI : 546
Seqid4 :R..... : 543

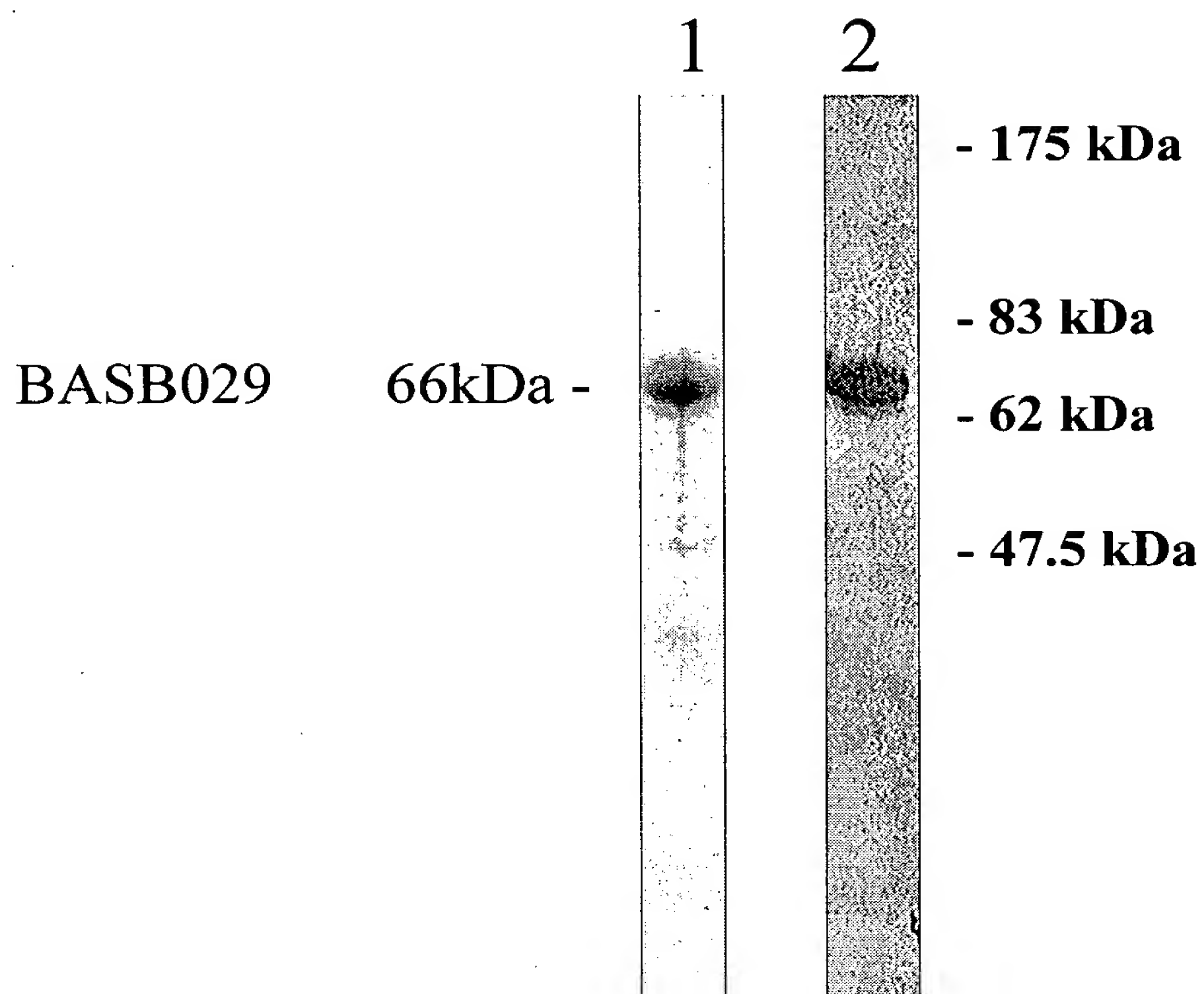
560 * 580 *
Seqid2 : GGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW : 594
Seqid4 : : 591

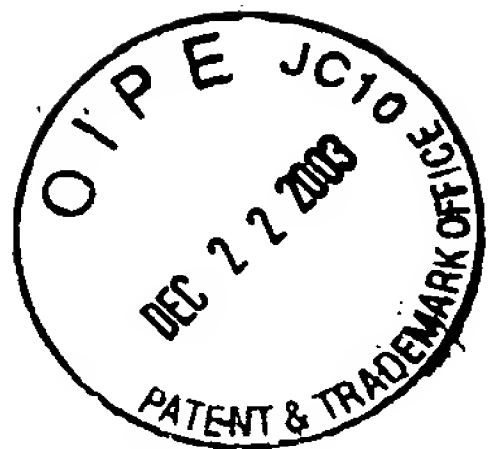


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Figure 3

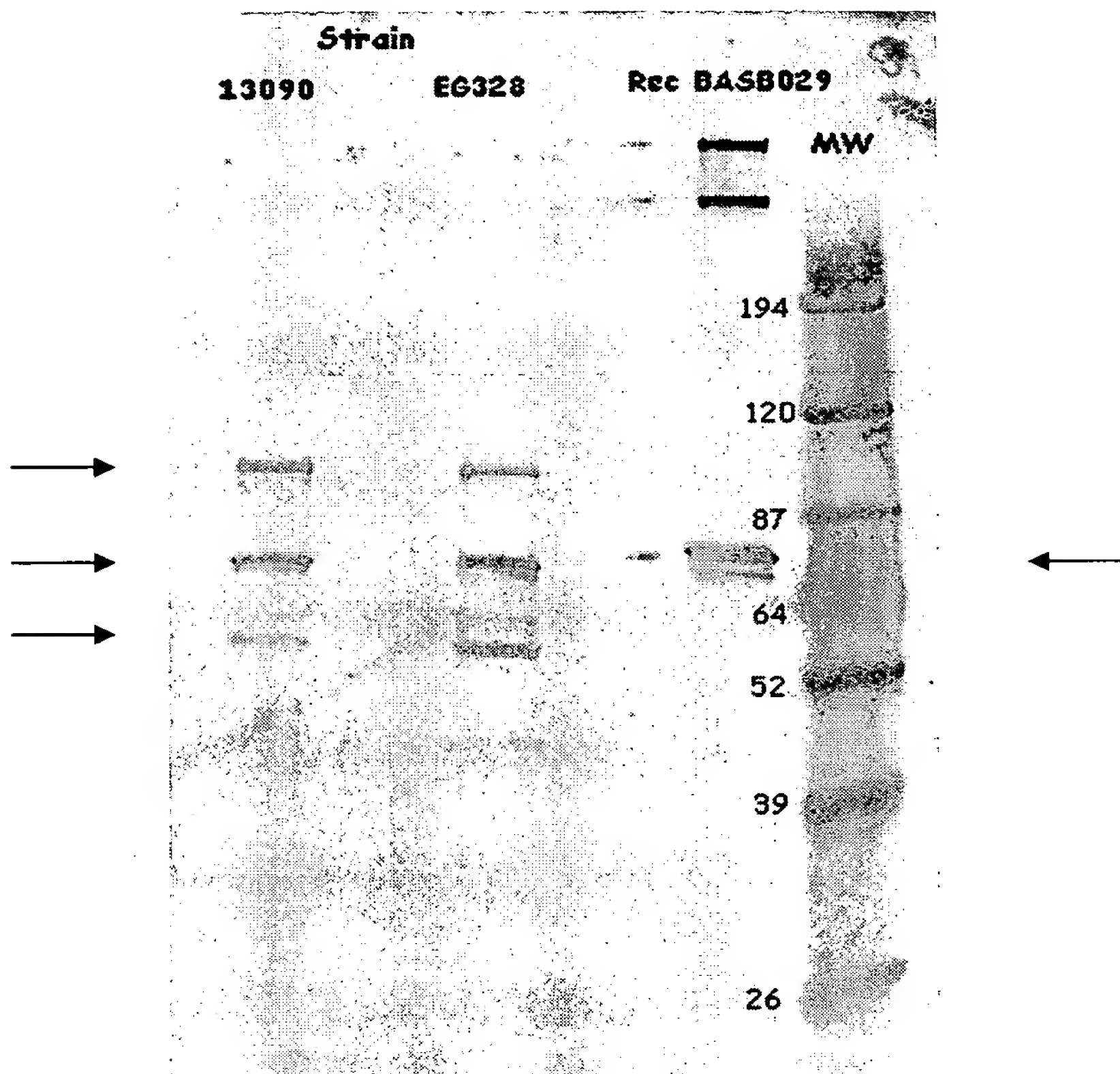


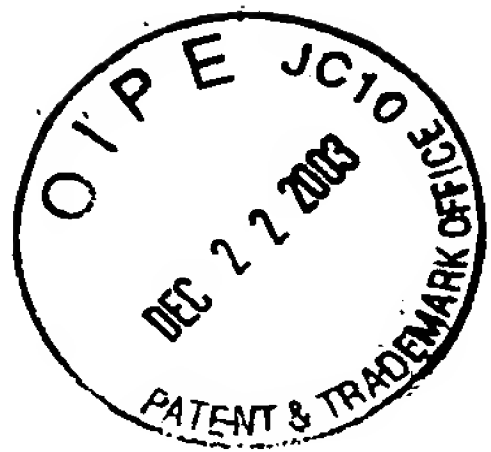


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Figure 4

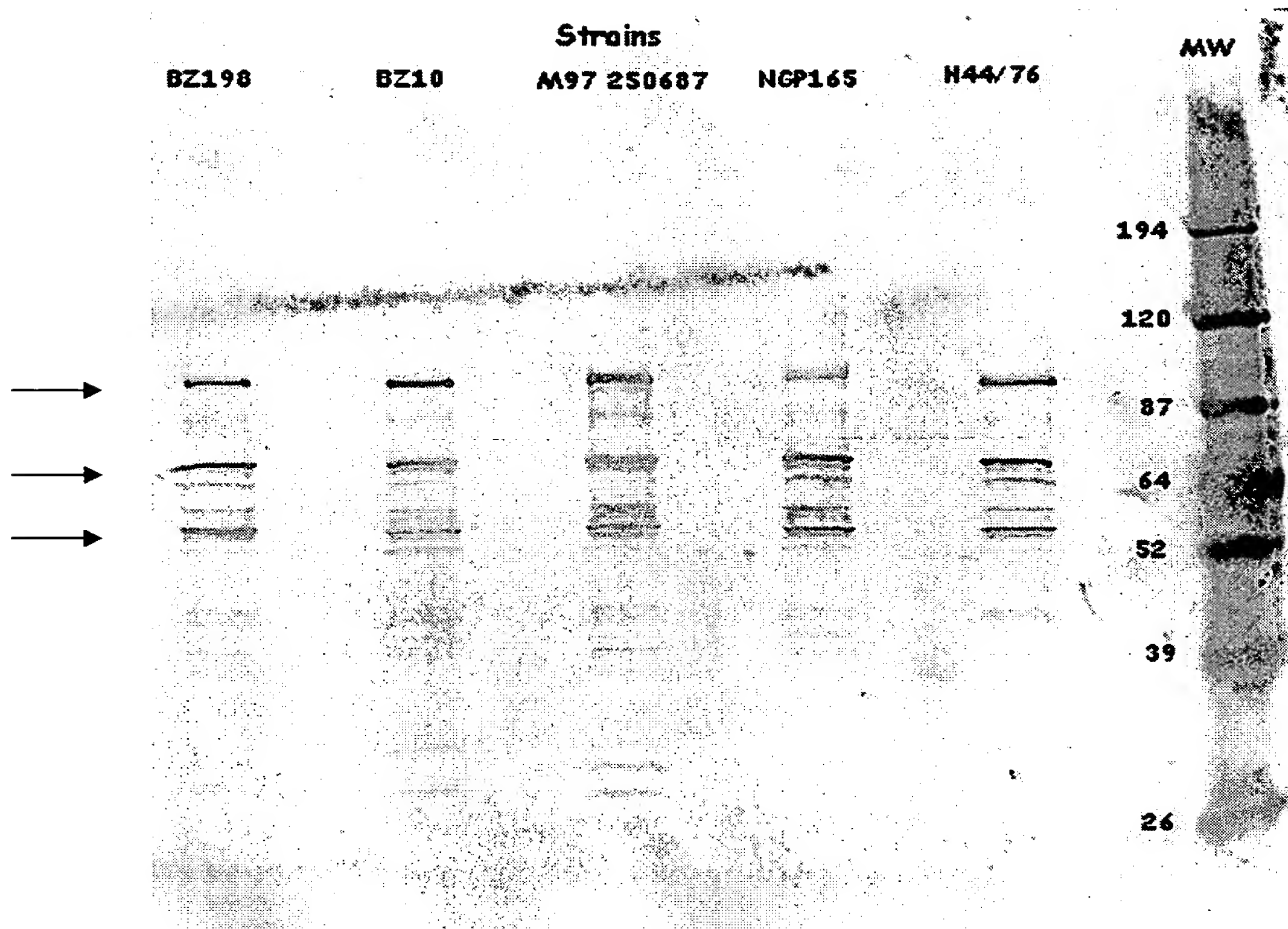


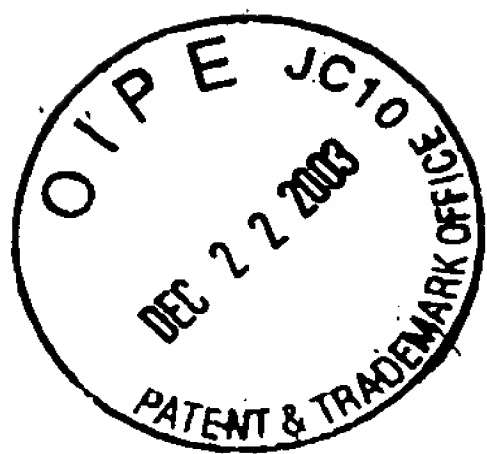


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Figure 5

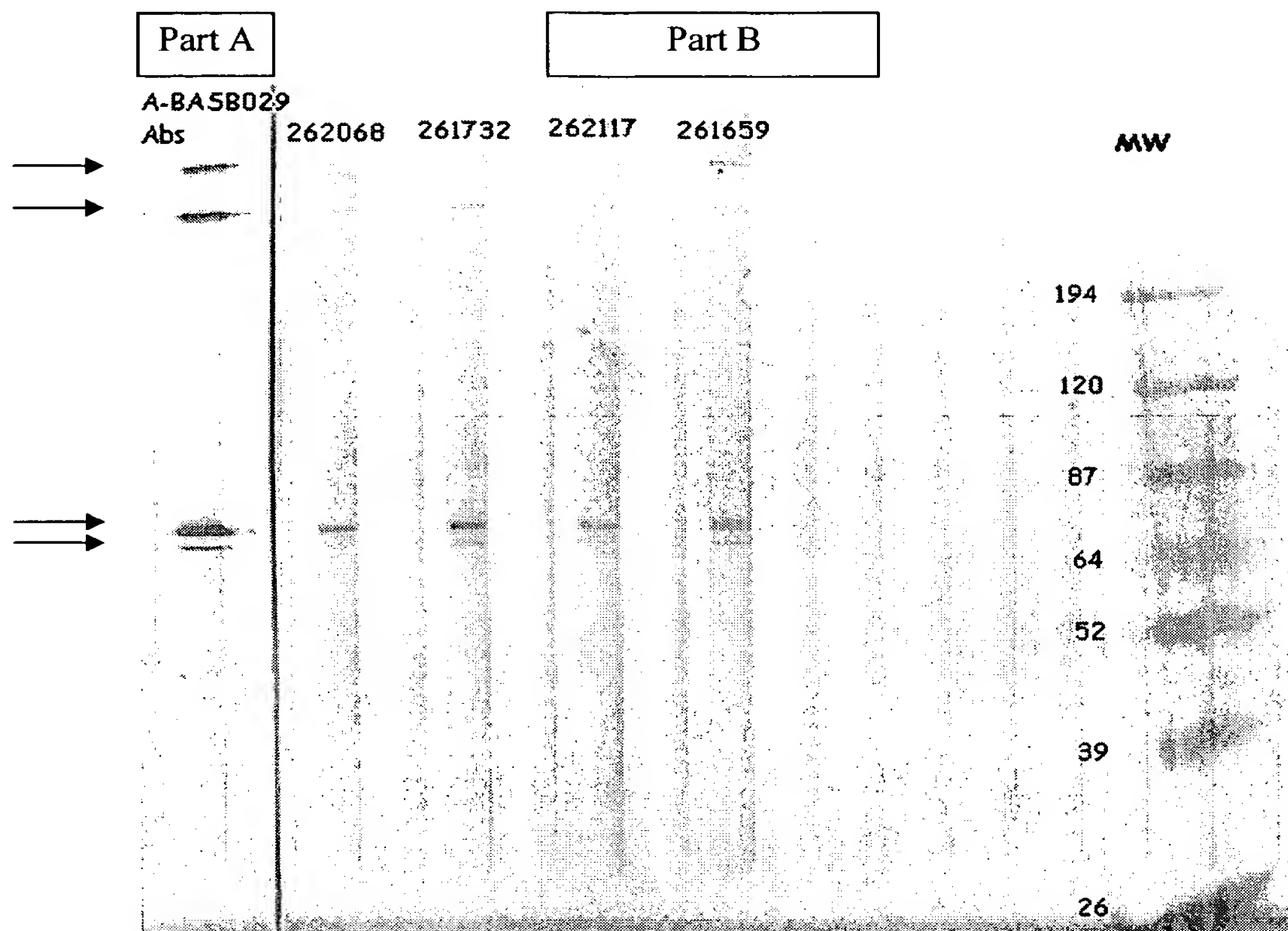


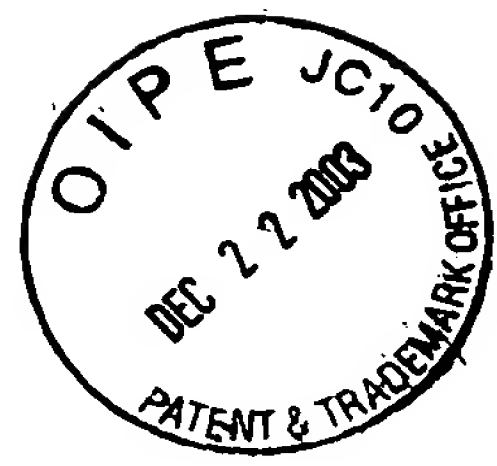


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Figure 6





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Figure 7

